

# SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> RuvB Polypeptides and Uses Thereof

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<151> 1999-07-16

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Ser Glu Val Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala  
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155 160 165

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 Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu  
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Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly Leu							
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Asp Ala Asn Gly Met Ser Met Pro Leu Ala Ala Gly Phe Val Gly Gln							
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Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg Gln							
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gtc cca ttc tgt cct atg gta gga tca gaa gtg tac tcc tca gag gtc Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Ser Glu Val 95 100 105	399
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cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt att gaa ctt Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val Ile Glu Leu 125 130 135	495
tcc cca gaa gag gct gag agc aca act ggt gga tat gcg aaa agc att Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile 140 145 150	543
agc cac gta atc att ggc tta aag act gtc aaa ggg act aag caa ttg Ser His Val Ile Ile Gly Leu Lys Thr Val Lys Gly Thr Lys Gln Leu 155 160 165 170	591
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caa ggt ggc caa gat att ttg tcc ctt atg ggc cag atg atg aag cca Gln Gly Gly Gln Asp Ile Leu Ser Leu Met Gly Gln Met Met Lys Pro 255 260 265	879
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Phe	Ala	Thr	Glu	Tyr	Asp	Leu	Glu	Ala	Glu	Glu	Tyr	Val	Pro	Ile	Pro	
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Ser	Pro	Leu	Ser	Pro	Ile	Val	Ile	Leu	Ala	Thr	Asn	Arg	Gly	Ile	Cys	
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Asn	Val	Arg	Gly	Thr	Asp	Met	Thr	Ser	Pro	His	Gly	Ile	Pro	Val	Asp	
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Ser	Leu	Arg	His	Ala	Ile	Gln	Leu	Leu	Ser	Pro	Ala	Ser	Val	Val	Ala	
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Lys	Thr	Asn	Gly	Arg	Glu	Lys	Met	Cys	Lys	Ala	Asp	Leu	Glu	Glu	Val	

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 Met Arg Ile Glu  
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 Ala Ala Gly Phe Val Gly Gln Ala Ala Ala Arg Glu Ala Ala Gly Leu  
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 Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg Ala Leu Leu  
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 70 75 80  
  
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108

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35 40 45	
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65 70 75	
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115 120 125	
agt aca act ggt gga tat gca aaa agc att agc cat gta atc atc agc Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile Ser	492
130 135 140	
tta aag act gtt aaa ggg act aag caa ctg aag tta gat tct tca att Leu Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Ser Ser Ile	540
145 150 155	
tat gat gct ctg atc aag gaa aag gtg gca gtg ggt gat gtt ata tac Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr	588
160 165 170 175	
atc gaa gca aat agt gga gca gtg aaa aga gtt ggt aga tgt gat tct Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser	636
180 185 190	
ttt gct aca gaa tac gat ctt gaa gct gaa gag tat gtt cct atc ccc Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro	684
195 200 205	
aaa ggt gaa gtc cat aag aaa aaa gaa att gtg cag gat gtc aca ctt Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu	732
210 215 220	
cat gac ctt gat gca gca aat gct cag cca caa ggt ggc caa gat att His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile	780
225 230 235	



ttg tcc ctt atg ggc cag atg atg aaa cca cga aag act gaa atc acc	828
Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr	
240 245 250 255	
 gaa aaa cta cgc caa gaa att aat aag gtg gta aat aga tat atc gat	876
Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp	
260 265 270	
 gaa gga att gca gag ctt gta cct ggt gtt ttg ttc att gat gag gtc	924
Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val	
275 280 285	
 cac atg ttg gat atc gaa tgt ttt tct tat ctt aac cgt gca ttg gag	972
His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu	
290 295 300	
 agc cca tta tca cca atc gtg ata ctt gct aca aat agg gga ata tgt	1020
Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys	
305 310 315	
 aat gta aga gga act gat atg aca agt cca cat ggt ata ccg gtg gat	1068
Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val Asp	
320 325 330 335	
 ctt cta gat agg ctg gtg att att cgg aca gag aca tat ggc cct act	1116
Leu Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro Thr	
340 345 350	
 gag atg ata cag ata ttg gct atc cga gca caa gtg gag gag att gat	1164
Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp	
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 atg gat gaa gaa agt ctt gct tat tta ggc gag atc gga cag cag aca	1212
Met Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr	
370 375 380	
 tct ttg aga cat gct att caa ttg ata tca cct gcc agc gtg gtc tca	1260
Ser Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser	
385 390 395	
 aag act aat gga aga gag aaa atc tgc aag gct gat ctc gag gaa gtt	1308
Lys Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val	
400 405 410 415	
 agt ggg ctc tat ttg gat gcc aaa tcc tcg gct cgg ctg ctc cag gag	1356
Ser Gly Leu Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu	
420 425 430	
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Gln Gln Glu Arg Tyr Ile Thr	
435	
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 <213> Zea mays

<400> 10

Met	Arg	Ile	Glu	Glu	Val	Gln	Ser	Thr	Ser	Lys	Lys	Gln	Arg	Ile	Ala	1	5	10	15
Thr	His	Thr	His	Ile	Lys	Gly	Leu	Gly	Leu	Asp	Ala	Asn	Gly	Met	Ala	20	25	30	35
Ile	Ala	Leu	Ala	Ala	Gly	Phe	Val	Gly	Gln	Lys	Lys	Met	Ala	Gly	Arg	40	45	50	55
Ala	Val	Leu	Leu	Ala	Gly	Pro	Pro	Ala	Thr	Gly	Lys	Thr	Ala	Leu	Ala	60	65	70	75
Gly	Ile	Ala	Gln	Glu	Leu	Gly	Ser	Lys	Val	Pro	Phe	Cys	Pro	Met	Val	80	85	90	95
Gly	Ser	Glu	Val	Tyr	Ser	Ser	Glu	Val	Lys	Lys	Thr	Glu	Val	Leu	Met	100	105	110	115
Glu	Asn	Phe	Arg	Arg	Ala	Ile	Gly	Leu	Arg	Ile	Lys	Glu	Asn	Lys	Glu	120	125	130	135
Val	Tyr	Glu	Gly	Glu	Val	Thr	Glu	Leu	Ser	Pro	Glu	Glu	Ala	Glu	Ser	140	145	150	155
Thr	Thr	Gly	Gly	Tyr	Ala	Lys	Ser	Ile	Ser	His	Val	Ile	Ile	Ser	Leu	160	165	170	175
Lys	Thr	Val	Lys	Gly	Thr	Lys	Gln	Leu	Lys	Leu	Asp	Ser	Ser	Ile	Tyr	180	185	190	195
Asp	Ala	Leu	Ile	Lys	Glu	Lys	Val	Ala	Val	Gly	Asp	Val	Ile	Tyr	Ile	200	205	210	215
Glu	Ala	Asn	Ser	Gly	Ala	Val	Lys	Arg	Val	Gly	Arg	Cys	Asp	Ser	Phe	220	225	230	235
Ala	Thr	Glu	Tyr	Asp	Leu	Glu	Ala	Glu	Glu	Tyr	Val	Pro	Ile	Pro	Lys	240	245	250	255
Gly	Glu	Val	His	Lys	Lys	Lys	Glu	Ile	Val	Gln	Asp	Val	Thr	Leu	His	260	265	270	275
Asp	Leu	Asp	Ala	Ala	Asn	Ala	Gln	Pro	Gln	Gly	Gly	Gln	Asp	Ile	Leu	280	285	290	295
Ser	Leu	Met	Gly	Gln	Met	Met	Lys	Pro	Arg	Lys	Thr	Glu	Ile	Thr	Glu	300	305	310	315
Lys	Leu	Arg	Gln	Glu	Ile	Asn	Lys	Val	Val	Asn	Arg	Tyr	Ile	Asp	Glu	320	325	330	335
Gly	Ile	Ala	Glu	Leu	Val	Pro	Gly	Val	Leu	Phe	Ile	Asp	Glu	Val	His	340	345	350	

Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp Met  
 355 360 365  
 Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr Ser  
 370 375 380  
 Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser Lys  
 385 390 395 400  
 Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val Ser  
 405 410 415  
 Gly Leu Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu Gln  
 420 425 430  
 Gln Glu Arg Tyr Ile Thr  
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<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based upon an adaptor  
 used for cDNA library construction and poly(dT) to  
 remove clones which have a poly(A) tail but no  
 cDNA insert.

<400> 11

tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa

36